

10/777,288

<!--StartFragment--> GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 14:02:40 ; Search time 7317 Seconds  
(without alignments)  
11247.824 Million cell updates/sec

Title: US-10-777-288A-899  
Perfect score: 1287  
Sequence: 1 gacatctccgtttccctccc.....aaagttaactgactatatg 1287

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : GenEmbl:\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_htg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1287	100.0	1287	2	CQ850430	CQ850430 Sequence
2	1287	100.0	1287	5	AK127564	AK127564 Homo sapi
3	1283.8	99.8	1370	5	BC073975	BC073975 Homo sapi
4	1062.2	82.5	1496	5	BC016167	BC016167 Homo sapi
5	1062.2	82.5	1556	5	BC064397	BC064397 Homo sapi
6	943.4	73.3	1246	14	BC109937	BC109937 Bos tauru
7	721.2	56.0	1202	6	BC088194	BC088194 Rattus no
8	588.8	45.7	893	6	BC100355	BC100355 Mus muscu
9	487.8	37.9	179531	14	CR933563	CR933563 Wallaby D
10	474	36.8	546	2	CQ722465	CQ722465 Sequence
11	405.2	31.5	29862	5	AL662798	AL662798 Human DNA
12	405.2	31.5	39659	12	CR847874	CR847874 Homo sapi
13	405.2	31.5	71418	5	AL732442	AL732442 Human DNA
14	405.2	31.5	88815	5	CR759778	CR759778 Human DNA
15	405.2	31.5	104755	5	BX908728	BX908728 Human DNA
16	405.2	31.5	105135	5	CR753328	CR753328 Human DNA
c 17	405.2	31.5	110000	5	BA000025_12	Continuation (13 o
c 18	405.2	31.5	110000	5	BA000041_08	Continuation (9 of
19	405.2	31.5	112118	5	BX119957	BX119957 Human DNA
c 20	405.2	31.5	123554	5	AB023049	AB023049 Homo sapi

21	405.2	31.5	130755	5	AL845353	AL845353 Human DNA
22	405.2	31.5	151228	5	AL662800	AL662800 Human DNA
23	405.2	31.5	310542	12	CR752729	CR752729 Homo sapi
24	405.2	31.5	349980	2	CS039417	CS039417 Sequence
25	396	30.8	404	2	AX070414	AX070414 Sequence
c 26	395.6	30.7	110000	5	AB128049_17	Continuation (18 o
27	395.6	30.7	174766	5	AC148659	AC148659 Macaca mu
28	335	26.0	114375	14	AB113357	AB113357 Sus scrof
29	335	26.0	146382	14	AB113356	AB113356 Sus scrof
30	325.2	25.3	473	2	AX982153	AX982153 Sequence
31	325.2	25.3	473	2	BD117012	BD117012 EST and e
32	325.2	25.3	473	2	AR421459	AR421459 Sequence
c 33	302	23.5	634	7	BV238118	BV238118 S234P6240
34	300.8	23.4	504	6	BC058418	BC058418 Mus muscu
c 35	286.8	22.3	437	2	AX335791	AX335791 Sequence
c 36	286.8	22.3	437	2	AX409947	AX409947 Sequence
c 37	285.6	22.2	153274	12	AY555280	AY555280 Mus muscu
38	282.4	21.9	172747	6	AC112970	AC112970 Mus muscu
c 39	282.4	21.9	188873	6	CR974451	CR974451 Mouse DNA
40	273.8	21.3	300	2	BD219935	BD219935 Human gen
c 41	269.4	20.9	349980	2	AX344571	AX344571 Sequence
c 42	269.4	20.9	349980	2	AX344572	AX344572 Sequence
43	253.2	19.7	297409	12	AC096275	AC096275 Rattus no
c 44	253.2	19.7	349943	6	BX883048	BX883048 Rattus no
c 45	229	17.8	21070	5	AB202095	AB202095 Homo sapi
c 46	229	17.8	21071	5	AB088098	AB088098 Homo sapi
47	189.6	14.7	192	2	AX905901	AX905901 Sequence
48	189.6	14.7	192	2	BD041434	BD041434 Sequence
49	189.6	14.7	192	2	AR741695	AR741695 Sequence
50	175.6	13.6	349980	2	AX344552	AX344552 Sequence

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 13:59:52 ; Search time 918 Seconds  
(without alignments)  
9774.819 Million cell updates/sec

Title: US-10-777-288A-899  
Perfect score: 1287  
Sequence: 1 gacatctccgtttccctccc.....aaagttaaactgactatatg 1287

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1287	100.0	1287	13	ADR07393	Adr07393 Full leng
2	1219.8	94.8	1223	12	ADQ87293	Adq87293 Human tum
3	1219.8	94.8	1223	12	ADQ83838	Adq83838 Human tum
4	1059.6	82.3	1243	8	ABX05085	Abx05085 Human nov
5	443.8	34.5	591	13	ADQ53687	Adq53687 Novel can
6	396	30.8	404	5	AAF65130	Aaf65130 Novel hum
7	392	30.5	400	9	ACH16377	Ach16377 Human adu
c 8	298.8	23.2	2036	4	AAD05547	Aad05547 Human sec
9	296.6	23.0	491	14	ADZ61349	Adz61349 Rat g2936
c 10	286.8	22.3	437	6	ABL67963	Abl67963 Ovary can
c 11	286.8	22.3	437	6	ABN96096	Abn96096 Gene #259
c 12	279.8	21.7	457	10	ABT41359	Abt41359 Toxicity
13	273.8	21.3	300	3	AAA01057	Aaa01057 Human col
14	189.6	14.7	192	3	AAC17689	Aac17689 Human sec
c 15	117	9.1	644	5	AAS34255	Aas34255 Human cDN
c 16	70.4	5.5	3133	10	ADC86738	Adc86738 Human GPC
c 17	69.2	5.4	629	13	ACN54594	Acn54594 Cotton an
c 18	69	5.4	3163	10	ADC87060	Adc87060 Human GPC
19	68.8	5.3	28198	10	ADG37080	Adg37080 Mouse pla
20	68.4	5.3	563	5	AAS34384	Aas34384 Human cDN

c	21	66	5.1	5452	10	ADC86736	Adc86736 Human GPC
c	22	65.2	5.1	12733	6	ABK98631	Abk98631 Vector pE
c	23	65.2	5.1	12733	9	ACD13882	Acd13882 L. lactis
c	24	65.2	5.1	12739	6	ABK98592	Abk98592 Vector pE
c	25	65.2	5.1	12739	9	ACD13843	Acd13843 Plasmid p
c	26	65	5.1	1117	10	ADC86688	Adc86688 Human GPC
c	27	64	5.0	588	13	ACN54596	Acn54596 Cotton an
	28	64	5.0	1064	6	ABT09678	Abt09678 Human PAL
	29	62	4.8	500	12	ADP85918	Adp85918 Synthetic
c	30	60.2	4.7	40772	13	ADW39403	Adw39403 Herpes si
c	31	60	4.7	1000	3	AAA02484	Aaa02484 Human col
	32	58.8	4.6	1337	2	AAZ17263	Aaz17263 Human gen
c	33	58.4	4.5	931	11	ACN87435	Acn87435 Breast ca
	34	58.4	4.5	1065	6	ABT09682	Abt09682 Human PAL
	35	57.4	4.5	600	6	ABQ52497	Abq52497 Oligonucl
c	36	57.4	4.5	600	6	ABQ52496	Abq52496 Oligonucl
c	37	57.4	4.5	1459	3	AAA02528	Aaa02528 Human col
	38	56.4	4.4	406	13	ACN59490	Acn59490 Cotton gy
	39	56.2	4.4	53522	6	AAD30228	Aad30228 Human PKD
	40	56.2	4.4	53522	13	ADU03973	Adu03973 Human pol
	41	56.2	4.4	53522	14	AEB35216	Aeb35216 Human Gef
	42	56.2	4.4	53526	2	AAT94101	Aat94101 Human PKD
	43	56.2	4.4	53577	2	AAT18551	Aat18551 Human pol
	44	56.2	4.4	53577	2	AAT94108	Aat94108 Human PKD
	45	56	4.4	4897	2	AAQ03259	Aaq03259 Pseudorab
c	46	55.2	4.3	1416	8	ABZ20967	Abz20967 Animal te
	47	55	4.3	987	6	ABT09669	Abt09669 Human PAL
c	48	54.6	4.2	795	2	AAV55830	Aav55830 FLGA inse
	49	54	4.2	478	13	ACN51281	Acn51281 Cotton an
c	50	54	4.2	799	2	AAV55831	Aav55831 Nucleotid

<!--EndFragment-->

<!--StartFragment-->GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 3, 2006, 14:10:30 ; Search time 6938 Seconds  
(without alignments)  
10373.044 Million cell updates/sec

Title: US-10-777-288A-899  
Perfect score: 1287  
Sequence: 1 gacatctccgtttccctccc.....aaagttaactgactatatg 1287

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_htc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
c	1	883	68.6	985	4	BX340635	BX340635 BX340635
	2	872.8	67.8	876	14	DQ054028	DQ054028 Homo sapi
	3	854.2	66.4	876	14	DQ054029	DQ054029 Pan trogl
	4	846	65.7	1094	3	BM558827	BM558827 AGENCOURT
	5	796.8	61.9	1060	2	BM551645	BM551645 AGENCOURT
	6	730.4	56.8	915	3	BQ954823	BQ954823 AGENCOURT
	7	724.2	56.3	1097	3	BM926246	BM926246 AGENCOURT
	8	721.8	56.1	869	3	BP165929	BP165929 BP165929
	9	709.8	55.2	1288	6	AK145087	AK145087 Mus muscu
	10	709.4	55.1	1151	6	AK172070	AK172070 Mus muscu
	11	702.4	54.6	2082	6	AK038622	AK038622 Mus muscu
	12	675	52.4	675	9	DR157885	DR157885 HESC2_83
c	13	674.8	52.4	739	3	BM677371	BM677371 UI-E-E01-
	14	656.2	51.0	694	2	BI765223	BI765223 603050308
c	15	649.4	50.5	662	7	BF221823	BF221823 7p37b09.x
	16	628.6	48.8	669	2	BI763966	BI763966 603049847
c	17	626.2	48.7	679	7	BF224092	BF224092 7q83g03.x
	18	625.8	48.6	820	9	DN107093	DN107093 1104510 M
c	19	623.8	48.5	819	9	DN106729	DN106729 1104126 M
	20	610.6	47.4	746	10	DT837916	DT837916 LB00441.C
	21	608.8	47.3	746	9	DN871473	DN871473 nad13f12.

	22	594.4	46.2	742	8	CO889119	CO889119	BovGen_17
c	23	589.8	45.8	612	3	BU679422	BU679422	UI-CF-DU1
	24	587.2	45.6	667	2	BI764214	BI764214	603046086
c	25	578.2	44.9	781	9	CX991484	CX991484	DOG_EST_P
	26	576	44.8	576	5	CK825958	CK825958	ik36f08.x
	27	571	44.4	571	9	DA444680	DA444680	DA444680
	28	570.2	44.3	739	6	AY610091	AY610091	Sus scrof
	29	559.8	43.5	806	8	CX218593	CX218593	MNS33196
c	30	550.4	42.8	595	5	CK825959	CK825959	ik36f08.y
	31	546.2	42.4	892	5	CF617102	CF617102	AGENCOURT
	32	546	42.4	976	3	BU513239	BU513239	AGENCOURT
c	33	544	42.3	544	9	DB313908	DB313908	DB313908
c	34	541.2	42.1	749	4	CB321830	CB321830	UI-CF-EN1
	35	535.4	41.6	595	7	AW967384	AW967384	EST379459
	36	535.4	41.6	668	5	CF358996	CF358996	818572 MA
	37	533	41.4	908	5	CF618737	CF618737	AGENCOURT
	38	530	41.2	720	10	DT719601	DT719601	LB0111.CR
	39	526.8	40.9	644	5	CK956234	CK956234	4096335 B
	40	523.8	40.7	527	3	BQ417335	BQ417335	ik36f08.y
	41	521	40.5	521	3	BM790196	BM790196	K-EST0069
c	42	515.4	40.0	518	1	AI143133	AI143133	qb76d09.x
	43	514.2	40.0	627	2	BI837701	BI837701	603086558
	44	512	39.8	773	8	CX239247	CX239247	NMA07043
	45	511.8	39.8	842	4	CA459080	CA459080	AGENCOURT
	46	510.2	39.6	649	5	CK946125	CK946125	4070565 B
	47	509	39.5	631	8	CO894259	CO894259	BovGen_22
	48	507.6	39.4	514	5	CD674180	CD674180	fs07e12.y
	49	504.6	39.2	860	8	CX200108	CX200108	MNS00694
c	50	502	39.0	510	7	BF590482	BF590482	7h35g05.x

<!--EndFragment-->

```
<!--StartFragment-->GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 3, 2006, 14:33:07 ; Search time 46.7 Seconds  
(without alignments)  
3780.113 Million cell updates/sec

Title: US-10-777-288A-899  
Perfect score: 2348  
Sequence: 1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10777288/runat\_03112006\_105409\_8336/app\_query.fasta\_1  
-DB=A\_Geneseq -QFMT=fastan -SUFFIX=n2p.100aligns.rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=300 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=100  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10777288\_CGN\_1\_1\_364@runat\_03112006\_105409\_8336  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq 8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1728	73.6	315	8	ADR09349	Adr09349 Human pro
2	907	38.6	172	6	ABG99987	Abg99987 Human nov
3	243.5	10.4	238	4	ABB68306	Abb68306 Drosophil
4	240	10.2	598	4	ABG14000	Abg14000 Novel hum
5	240	10.2	598	7	ADF60423	Adf60423 Human con
6	219.5	9.3	1216	8	ADX97588	Adx97588 Pancreati
7	219.5	9.3	1250	6	AAO26231	Aao26231 MDDT rela
8	219.5	9.3	1250	8	ADM87156	Adm87156 Human pro
9	209	8.9	763	2	AAW31852	Aaw31852 Mycobacte
10	207.5	8.8	693	7	ADM05164	Adm05164 Human pro

11	207.5	8.8	693	9	AEC88094	Aec88094 Human cDN
12	204.5	8.7	693	5	ABP69529	Abp69529 Human pol
13	203.5	8.7	1008	4	ABB11527	Abb11527 Human apo
14	200	8.5	406	4	ABG27250	Abg27250 Novel hum
15	199	8.5	446	4	ABB70063	Abb70063 Drosophil
16	199	8.5	1579	8	ADS97981	Ads97981 Protein f
17	199	8.5	2161	7	ADJ69477	Adj69477 Human hea
18	199	8.5	2161	9	ADX98562	Adx98562 Human SH3
19	198.5	8.5	598	6	ABU37030	Abu37030 Protein e
20	198.5	8.5	1013	4	ABG08112	Abg08112 Novel hum
21	198	8.4	572	2	AAW31855	Aaw31855 Mycobacte
22	196.5	8.4	313	8	ABO59570	Abo59570 Human gen
23	193.5	8.2	1315	2	AAW76734	Aaw76734 Human mDi
24	193.5	8.2	1616	8	ADP22958	Adp22958 PRO polyp
25	192	8.2	800	8	ABO58564	Abo58564 Human gen
26	191.5	8.2	1248	2	AAy13464	Aay13464 Human dia
27	191.5	8.2	1567	5	ABB99164	Abb99164 Mouse for
28	191.5	8.2	1567	7	ABW01569	Abw01569 Mouse for
29	191.5	8.2	1682	8	ADR14131	Adr14131 Human NF-
30	191	8.1	451	7	ADE62342	Ade62342 Rat Prote
31	190	8.1	639	8	ADN21309	Adn21309 Bacterial
32	188.5	8.0	681	5	ABB93650	Abb93650 Herbicida
c 33	188.5	8.0	684	4	ABG14126	Abg14126 Novel hum
34	187.5	8.0	1006	8	ADU20559	Adu20559 A. thalia
35	187.5	8.0	1006	8	ADU20561	Adu20561 A. thalia
36	187.5	8.0	1526	6	ABO14750	Abo14750 Novel hum
37	187	8.0	1413	5	AAE21729	Aae21729 Human PKI
38	186	7.9	694	5	ABB92421	Abb92421 Herbicida
39	185.5	7.9	280	7	ABW01568	Abw01568 Mouse for
40	183	7.8	325	4	ABG21919	Abg21919 Novel hum
41	183	7.8	386	9	ADZ47759	Adz47759 Mycobacte
42	183	7.8	2091	3	AAB12000	Aab12000 Rat p3103
43	182.5	7.8	1313	7	ADJ70374	Adj70374 Human hea
44	181	7.7	707	9	ADZ44698	Adz44698 NFk-B pro
45	181	7.7	707	9	AEB31351	Aeb31351 Human PSF
46	180.5	7.7	525	9	AEB31354	Aeb31354 Human SFP
47	180.5	7.7	669	9	AEB31352	Aeb31352 Human PSF
48	180.5	7.7	707	4	AAM39141	Aam39141 Human pol
49	180.5	7.7	707	7	ADE54941	Ade54941 Human Pro
50	180.5	7.7	707	7	ADE54938	Ade54938 Human Pro

&lt;!--EndFragment--&gt;



&lt;!--StartFragment--&gt;

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 3, 2006, 14:44:57 ; Search time 11.1 Seconds  
(without alignments)  
3346.783 Million cell updates/sec

Title: US-10-777-288A-899  
Perfect score: 2348  
Sequence: 1 gacatctccgtttccctccc.....aaagtttaactgactatatg 1287

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10777288/runat\_03112006\_105413\_8382/app\_query.fasta\_1  
-DB=PIR -QFMT=fastan -SUFFIX=n2p.100aligns.rpr -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=300 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=100  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10777288\_CGN\_1\_1\_71@runat\_03112006\_105413\_8382 -NCPU=6  
-ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_80:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	203.5	8.7	839	2 T04859	extensin homolog F
2	190.5	8.1	577	2 T09024	proline-rich prote
3	187.5	8.0	1006	2 G86292	hypothetical prote
4	185.5	7.9	1690	2 T31670	DNA-directed RNA p
5	181.5	7.7	530	2 A45690	transactivator EBN
c 6	181.5	7.7	682	2 T28899	hypothetical prote
7	181	7.7	990	2 T14756	hypothetical prote
8	180.5	7.7	707	2 A46302	PTB-associated spl
9	180	7.7	416	2 T34279	hypothetical prote
10	180	7.7	1184	2 G01763	atrophin-1 - human
c 11	179.5	7.6	274	2 T25404	hypothetical prote
12	179	7.6	464	2 S22697	extensin - Volvox
13	178	7.6	376	2 S71558	probable cell wall
14	178	7.6	1184	2 S50832	atrophin-1 - human
c 15	177.5	7.6	375	2 JS0427	S-antigen precurs

16	176.5	7.5	786	2	T01456	extensin homolog F
17	176.5	7.5	1255	2	T31065	diaphanous protein
18	176	7.5	473	2	S50755	hypothetical prote
19	176	7.5	708	2	D96711	hypothetical prote
20	174.5	7.4	1188	2	S49915	extensin-like prot
21	174	7.4	1357	2	T29265	hypothetical prote
c 22	173	7.4	1549	2	I48103	type VII collagen
23	172	7.3	1494	2	T14355	protein-tyrosine-p
24	171.5	7.3	350	2	S22456	hydroxyproline-ric
25	171.5	7.3	1611	2	T38236	hypothetical prote
26	171	7.3	666	2	B70803	hypothetical prote
27	171	7.3	1541	2	T02831	AAA protein L4171.
28	170	7.2	620	2	S06733	hydroxyproline-ric
c 29	170	7.2	1489	2	D70807	hypothetical glyci
30	170	7.2	3020	2	A43932	mucin 2 precursor,
31	169.5	7.2	1520	2	T00273	hypothetical prote
32	169	7.2	439	2	S51939	chitinase (EC 3.2.
33	169	7.2	760	2	F86387	probable Pto kinas
34	169	7.2	907	2	E96636	hypothetical prote
35	168.5	7.2	306	2	T52340	cell wall-plasma m
36	168	7.2	515	2	F70904	hypothetical prote
37	167.5	7.1	548	2	S59133	ETS2 repressor fac
c 38	167.5	7.1	1660	2	A70869	hypothetical glyci
39	167.5	7.1	1859	1	A34092	DNA-directed RNA p
40	167.5	7.1	1862	2	T29959	DNA-directed RNA p
41	167	7.1	449	2	S16748	proline-rich prote
42	167	7.1	915	2	T12526	hypothetical prote
43	167	7.1	5262	2	T03454	ALR protein - huma
c 44	166.5	7.1	346	1	S35500	heterogeneous ribo
c 45	166.5	7.1	584	2	G70804	hypothetical glyci
46	165.5	7.0	839	2	F75518	hypothetical prote
47	165.5	7.0	4957	2	T03455	ALR protein - huma
48	165	7.0	487	2	S42442	nuclear protein EB
49	165	7.0	744	2	E86255	hypothetical prote
50	165	7.0	1201	2	G86441	unknow<!--EndFragment-->

```
<!--StartFragment--> GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
```

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 3, 2006, 14:34:27 ; Search time 83 Seconds  
(without alignments)  
4302.994 Million cell updates/sec

Title: US-10-777-288A-899  
Perfect score: 2348  
Sequence: 1 gacatctccgtttccctccc.....aaagttaactgactatatg 1287

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Command line parameters:

```
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10777288/runat_03112006_105411_8347/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.100aligns.rup -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=300 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02p -USER=US10777288_CGN_1_1_684_@runat_03112006_105411_8347
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1716	73.1	315	1 CF136_HUMAN	Q5sqh8 homo sapien
2	1519	64.7	315	2 Q32KT5_BOVIN	Q32kt5 bos taurus
3	1267	54.0	338	2 Q3UM69_MOUSE	Q3um69 mus musculu
4	1256	53.5	326	2 Q3TA61_MOUSE	Q3ta61 mus musculu
5	880	37.5	172	1 CF136_MACMU	Q5tm64 macaca mula
6	792	33.7	172	1 CF136_RAT	Q6mg12 rattus norv
7	788	33.6	172	2 Q497V8_MOUSE	Q497v8 mus musculu
8	476	20.3	102	2 Q6PDX4_MOUSE	Q6pdx4 mus musculu
9	441	18.8	178	2 Q5PPL5_XENTR	Q5ppl5 xenopus tro
10	285.5	12.2	247	2 Q7PFX4_ANOGA	Q7pfx4 anopheles g
11	243.5	10.4	253	2 Q9W1F2_DROME	Q9w1f2 drosophila
12	239.5	10.2	253	2 Q8SYW2_DROME	Q8syw2 drosophila
13	234.5	10.0	3409	2 Q6SSE6_CHLRE	Q6sse6 chlamydomon
14	225	9.6	3889	2 Q6SSE8_CHLRE	Q6sse8 chlamydomon
15	219.5	9.3	1302	1 RAPH1_HUMAN	Q70e73 homo sapien
16	217.5	9.3	4027	2 Q5I2R0_CHLIN	Q5i2r0 chlamydomon
17	217	9.2	2371	2 Q58NA5_CHLIN	Q58na5 chlamydomon
18	212.5	9.1	2332	2 Q4A2B5_9PHYC	Q4a2b5 emiliana h

19	212	9.0	555	1	GP1_CHLRE	Q9fpq6	chlamydomon
20	210.5	9.0	1332	2	Q59GF6_HUMAN	Q59gf6	homo sapien
21	210.5	9.0	1865	2	Q5VU37_HUMAN	Q5vu37	homo sapien
22	210	8.9	665	2	Q2U6Q3_ASPOR	Q2u6q3	aspergillus
23	209	8.9	763	2	Q9XDH2_MYCTU	Q9xdh2	mycobacteri
24	207.5	8.8	585	2	O41935_MHV68	O41935	murid herpe
25	206.5	8.8	727	2	Q35LL9_9BRAD	Q35l19	bradyrhizob
26	206.5	8.8	745	2	Q89X06_BRAJA	Q89x06	bradyrhizob
27	206	8.8	516	2	Q4A2Z7_9PHYC	Q4a2z7	emiliana h
28	204.5	8.7	616	2	Q9H6K5_HUMAN	Q9h6k5	homo sapien
29	203.5	8.7	839	2	Q9SN46_ARATH	Q9sn46	arabidopsis
30	201.5	8.6	861	2	Q69JZ8_ORYSA	Q69jz8	oryza sativ
31	199	8.5	420	2	Q9VZC2_DROME	Q9vzc2	drosophila
32	199	8.5	2161	1	SHAN1_HUMAN	Q9y566	homo sapien
33	198.5	8.5	598	2	Q8VKN7_MYCTU	Q8vkn7	mycobacteri
34	198.5	8.5	676	2	Q95JC9_PIG	Q95jc9	sus scrofa
35	197.5	8.4	498	2	Q5KGJ5_CRYNE	Q5kgj5	cryptococcu
36	197	8.4	946	2	Q2R063_ORYSA	Q2r063	oryza sativ
37	197	8.4	2033	2	Q9E938_9ALPH	Q9e938	gallid herp
38	197	8.4	2033	2	Q9E940_9ALPH	Q9e940	gallid herp
39	195	8.3	3204	2	Q6X248_9ALPH	Q6x248	bovine herp
40	193.5	8.2	511	2	Q95JD0_PIG	Q95jd0	sus scrofa
41	193.5	8.2	566	2	Q95JD1_PIG	Q95jd1	sus scrofa
42	193.5	8.2	687	2	Q948Y7_VOLCA	Q948y7	volvox cart
43	193.5	8.2	1272	2	Q6URC4_HUMAN	Q6urc4	homo sapien
44	193.5	8.2	1299	2	Q59FH8_HUMAN	Q59fh8	homo sapien
45	191.5	8.2	410	2	Q7PZX2_ANOGA	Q7pzx2	anopheles g
46	191.5	8.2	1248	1	DIAP1_HUMAN	O60610	homo sapien
47	191.5	8.2	1567	1	FMN2_MOUSE	Q9j104	mus musculu
48	191.5	8.2	1682	2	O15054_HUMAN	O15054	homo sapien
49	191	8.1	309	2	Q8UZB4_9VIRU	Q8uzb4	grapevine f
50	191	8.1	451	2	Q62775_RAT	Q62775	rattus norv

&lt;!--EndFragment--&gt;